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Claim 1; Page

53; 64pp; English.

A human colon specific protein (AAW12691) is a potential diagnostic marker for colon cancer. It is believed that the presence of active transcription of the colon specific gene in non-colon cells of a host is indicative of colon cancer metastases. The amino acid sequence of the colon specific protein was deduced from a cDNA clone (AATS1784) isolated from a human colon cancer cDNA library. Recombinant colon specific protein can be produced in transformed host (e.g. bacterial, insect) cells and used to develop prods. for the diagnosis and treatment of colon disorders, partic. colon cancer metastasis. Antibodies raised against the protein can be used to target cancer cells and as part of a colon cancer

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                                   The present sequence represents a human Reg I-gamma protein, which comprises a C-type lectin. The sequence was identified in Incyte clone 131034. Reg I-gamma protein is involved in regulation of cell growth and development. Since the overexpression of reg proteins is associated with tumourogenesis and neurodegeneration, inhibition of human Reg I-gamma expression can be used for treating or preventing neoplasia or metastasis and neurodegenerative changes associated with Alzheimer's disease and other disorders of the central nervous system, e.g. Down's syndrome. Reg I-gamma can also be used in therapeutics to induce regeneration of pancreatic beta-cells in the treatment of diabetes. The products can also be used for detection for, e.g. expression of REG I-gamma, diagnosis and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; Reg I-gamma protein; C-type lectin; Incyte clone 1310334; regulation; cell growth; development; tuncurogenesis; neurodegeneration; inhibition; treatment; prevention; neoplasia; metastasis; neurodegenerative change; Alzheimer's disease; Down's syndrome; regeneration; pancreatic beta-cells; diabetes.
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                                                                                                                                                                                                                                                                                           This is the amino acid sequence of a novel human protein comprising a secretory signal isolated from stomach cancer cells. Its proteins can used as nutritional sources or supplements. The proteins may also have cytokine functions, immune modulating functions, haematopoiesis regulating activity, activin/inhibin regulating activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity receptor/ligand activity, anti-inflammatory activity, tumour inhibitions.
                                                                                                                                                                                                                Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ++
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yamaguchi T,
                                                                                                                                  100.0%;
                                                                                                         0;
                                                                                                                                  Score 878; DB 2;
Pred. No. 6.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 6., Mismatches
                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; tumour; chemotactic; chemokinet inhibition; stomach cancer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kobayashi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.8e-83;
                                                                                                                                                           Length 158;
                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to treat immune disorders, etc.
                                                                                                         <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                    ic activity, inhibition
                                                                                                         Gaps
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have
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                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is encoded by a human colon specific gene. The nucleic acid sequence can be used to develop products for the diagnosis of a disorder of the colon, e.g. colon cancer or metastases. The product can also be used to screen for agonists or antagonists for the polypeptides. The antagonists may be used to treat colon cancer, since they interact with the function of colon specific polypeptides to inhib functions which are necessary for the viability of colon cancer cells. The products can also be used for the production of antibodies and for the identification of receptors for the polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1A-C; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           metastases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated human colon specific gene - diagnosis and treatment of disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAX03195.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-130432/11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; colon specific gene; diagnosis; colon disorder; colon cancer; viability; colon cancer cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein encoded by a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW84274 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5861494~8
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                                                                                                                                                                                                              MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                 KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                        YGNGAHLASILSLKEASTIAEYISGYQRSQPJWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                                                                                             YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            colon specific gene.
                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                          Score 878; DB 2;;
Pred. No. 6.8e-83;
; Mismatches ;0;
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                                                                                                                                                                                                                                                                                                                                                                             Length 158;
                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 6
AAB74934
ID AAB7

AAB74934

standard;

protein;

158

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(first entry)

Human TSA7005 27-JUN-2001

protein SEQ

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                                                                                                                                                              Query Match
Best Local S
Matches 158
                                                                                                                                                                                                                                            This invention relates to a purified human protein, which is primarily expressed in tissue derived from the colon. The protein is 152 amino acids in length and exhibits cytostatic activity. The present sequence represents the amino acid sequence of the colon specific protein. The protein can be used in the diagnosis and treatment of colon cancer, and it is thought that abnormally high levels of the gene expression in non colon cells is an indication of colon cancer metastasis
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                            Claim 1; Fig 1; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                    Novel human colon specific polypeptides and polynucleotides for diagnosis and treatment of colon cancer, for screening compounds which interact with polypeptide, for synthesis of DNA and manufacture of DNA vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human colon specific protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN
121
                        121
                                                                                                                                                                158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PJ,
                                                                                                                                                                              Similarity
                                                                                                                                                                                                                       158
                                                                                                                             MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
              KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP
                                                    YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                      YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                                                          MASRSMRLLLLLLSCLAKTGVLGDI IMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific; colon cancer; metastasis; diagnose; treatment;
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                                                                                                                                                              Score 878; DB 3;
Pred. No. 6.8e-83;
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158
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ARESULT 7

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CB8C
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Best Local
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     30-DEC-1999;
10-JAN-2000;
15-FEB-2000;
                                                                                                          29-DEC-2000;
                                                                                                                                                               12-JUL-2001
                                                                                                                                                                                                               WO200149716-A2
                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                           C880P similar amino acid sequence (GENESEQ W37866).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAM24519 standard; protein; 158 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents a human TSA7005 protein which shares 32% homology with human and mouse Reg proteins, and 34% homology with the rat Reg protein. TSA7005 has pancreatic beta cell growth activity and hypoglycaemic activity. The TSA7005 protein can be used for the diagnosis and treatment of diseases associated with the gene and its expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TSA7005 gene, encoding a polypeptide useful for the diagnosis treatment of diseases associated with its expression.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999;
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                                                                                                                                                                                                                                                                                                              therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                         immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGMFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAF82117,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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  99US-00476296.
2000US-00480321.
2000US-00504629.
                                                                                                          2000WO-US035596.
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                   vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                   colonic
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Pred. No. 6.8e-83;
                                                                                                                                                                                                                                                                                                                   cancer.
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gene therapy;

C880P similar 12-OCT-2001

amino acid sequence

(GENÉSEQ W37929).

(first entry)

Human; immunotherapy; diagnosis;

vaccine; colonic.

s; colon cancer; colon tumour; immunogenic; cancer.

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RESULT 8
AAM24520
ID AAM2
XX
AC AAM2
AC AAM2
XX
DT 12-C
XX
DT 12-C
XX
DT C880
XX
KW Huma
KW gene
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCAPS by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins, by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used as diagnostic agents for detecting the antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (BLISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
28-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                χυ ď,
                                                                                                                                                                 AAM24520 standard; protein; 158 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 158 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colon tumor associated proteins and nucleic acids useful prevention, diagnosis and treatment of colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-441847/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytostatic activity, and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases (II) may be used in the prevention, diagnosis and treatment of diseases
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3E, Wang T,
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                                                                                                                                                                                                                                                                                                                                                                      YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
                                                                                                                                                                                                                                                                                               KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                                                               KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                                                                                                                                      YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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; 2000US-00575251.
; 2000US-00609448.
; 2000US-00649811.
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Jiang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          on describes colon (II) that encode t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                acid sequences given in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 878; DB 4;
Pred. No. 6.8e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 158;
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Homo sapiens

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                                                                                                                                                                                                                                                                               Query Match
Best Local
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10-JAN-2000;
15-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colon tumor associated proteins and nucleic acids useful for the prevention, diagnosis and treatment of colonic cancer.
                                                                                                                                                                                                                                                                                                                                              Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 2; Page 468; 472pp; English.
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29-JUN-2000;
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121
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E, Wang T,
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                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                         invention
                           KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                                                                                                       MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                   YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                                                                       YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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; 2000US-00504629.
; 2000US-00519444.
; 2000US-00575251.
; 2000US-00609448.
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Jiang Y;
                                                                                                                                                                                                                                                                            100.0%; Score 878; DB 4; 100.0%; Pred. No. 6.8e-83;
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                                                                                                                                                                                                                                                                                                 Length 158;
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RESULT 9
AAM24521
AAC
AAM24521
AAM2452
                                                          15-FEB-2000;
06-MAR-2000;
19-MAY-2000;
    Sequence 158 AA;
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                                                 present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 2; Page 469; 472pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colon tumor associated proteins and nucleic acids useful prevention, diagnosis and treatment of colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-441847/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Хu J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-DEC-1999;
10-JAN-2000;
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E, Wang T,
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2000US-00649811
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2000US-00504629.
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Jiang Y;
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Query Match
Best Local Similarity
Matches 158; Conserv

Conservative

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Score 878; DB 4; Pred. No. 6.8e-83;); Mismatches 0;

Length 158; Indels

0

Gaps

100.0%;

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RESULT 10
AAM24517
ID AAM24517
ID AAM24517
ID AAM24
XX AAM24
XX AAM24
XX AAM24
XX I2-OC
XX I2-OC
XX Human
XW Gene
XX Homo
XX Homo
XX Homo
XX Homo
XX I2-JU
XX 29-DE
XX 29-DE
XX 10-ME
PR 10-ME
PR 10-ME
PR 15-FE
P
                   The present invention describes colon tumour associated proteins (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) (I) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) (I) may be used to treat disorders associated with decreased expression by rectifying (I) and (II) may be used to treat disorders associated with decreased expression by rectifying (I) may be used to product the patients own (II) may be used to produce the TCAP (II) proteins or to supplement the patients own (II) proteins, by inserting the nucleic acids into a host cell culturing the (II) proteins, by inserting the nucleic acids into a host cell culturing the (II) to express the protein. (II) and its complementary sequences may (II) and its complementary sequences may (II) and by idiatation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs expression and activity. The anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies and activity. The anti-(II) antibodies and activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colon tumor associated proteins and prevention, diagnosis and treatment
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29-JUN-2000;
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15-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CS1-152 clone predicted amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-AUG-2000;
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E, Wang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunotherapy; diagnosis; colon cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 463; 472pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          в МJ,
q́т,
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2000US-00504629.
2000US-00519444.
2000US-00519444.
2000US-00575251.
2000US-00609448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diagnosis and
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Jiang Y;
   be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             colonic
as diagnostic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acids useful of colonic cancer.
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   agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Meagher MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       colon tumour; immunogenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             158
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   for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Stolk JA;
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RESULT 11
AAM24518
ID AAM24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-MAR-2000;
19-MAY-2000;
29-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  Xu J,
King (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immunou
gene therapy;
                                                                                                                                                                                                                                                                                    prevention,
                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-441847/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      presence of TCAPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAI28460 to AAI29512 and AAM24494 to AAM24523 represent nucleotide and amino acid sequences given in the exemplification of the
                                                                                                The present invention describes colon tumour associated proteins (I) and the polymucleotides (II) that encode them. (I) have cytostatic activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases
                                                                                                                                                                                                                                   Claim 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C880P similar amino acid sequence (GENESEQ W12691).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-AUG-2000;
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15-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                    tumor associated proteins and ntion, diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                               Lodes MJ,
3E, Wang T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
herapy; vaccine; colonic cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-00480321.
; 2000US-00504629.
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; 2000US-00609448.
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                                                                                                                                                                                                                                 467; 472pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9905-00476296
                                                                                                                                                                                                                                                                                                                                                                                                               Secrist H,
, Jiang Y;
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Pred. No. 6.8e-83
                                                                                                                                                                                                                                                                                                                                                                                                                                            Benson
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                                                                                                                                                                                                                                                                                      nucleic acids useful of colonic cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                            DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                            Meagher
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associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be to treat disorders associated with decreased expression by rectifyin

ession by rectifying affect the activity

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be used

mutations or deletions in a patient's genome

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RESULT 12
AAE29829
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 158;
Detecting the presence of a tumor comprises detecting the concentration of a Reg Like Protein or the presence or quantity of a nucleic acid
                                                                                WPI; 2002-684095/74.
N-PSDB; AAD47239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; REG-like protein; RELP; tumour; cancer; therapy; chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human REG-like protein (RELP).
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                                                                                                                                                                                                                                                                   16-MAR-2001;
                                                                                                                                                             Heiskala M;
                                                                                                                                                                                                                                                                                                                     15-MAR-2002; 2002EP-00251876
                                                                                                                                                                                                                                                                                                                                                                                                                           EP1241269-A2
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                                                                                                                                                                                                                                                                   2001US-0276414P
                                                                                                                                                                                                               CLINICAL DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Human mature REG-like protein"
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Pred. No. 6.8e-83;
); Mismatches 0;
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Best Local Simi
Matches 158;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Human; colon cancer; cancer; tissue profiling; forensic; genetic analysis; diagnostic; antisense therapy.
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ABQ56306 to ABQ60787 represent isolated nucleic acids (I) differentially expressed in cancer tissues. ABB78993 to ABB79004 represent proteins encoded by the ABQ60776 to ABQ60787 nucleic acid sequences. (I) can be
                                                                                      New isolated nucleic acid that is differentially expressed in cancer tissues useful for determining the presence of colon cancer in a cell or tissue type, and in antisense therapy.
                                                                                                                                                                                              Burgess C, Astle JH,
Thiaglingam A, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human Reg IV protein sequence SEQ ID NO:4471.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-AUG-2002
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                                                            Claim 5;
                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                            02-OCT-2000; 2000US-023727JP
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                                                                                                                                                    2002-426115/45.
DB; ABQ60776.
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                                                           Fig 3; 796pp; English.
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                                                                                                                                                                                                   Lewis
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Matches
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08-FEB-2002;
12-APR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                used in antisense therapy. An antibody immunoreactive with a polypeptide encoded by (I) is useful for detecting cancer in a patient sample, and for detecting the presence or absence of a polynucleotide encoded by a nucleic acid which hybridises to (I) in a cell. A probe/primer derived from (I) can be used for determining the presence of a nucleic acid which hybridises to (I), and for determining the phenotype of cells in a sample of cells from a patient. (I) is useful for determining the presence of colon cancer in a cell or tissue type, for determining the presence or state of other type of cancer, in antisense therapy, to generate macroarrays on a solid surface, to identify a chromosome on which the corresponding gene resides, and in tissue profiling, forensice, genetic analysis, mapping and diagnostic applications. (I) can be used to raise antibodies, and to screen for peptide analogues and antagonists
         New genes that are up-regulated or down-regulated in cancers, useful as markers for diagnosing e.g. cancer, ischemia or heart diseases, or as therapeutic targets for screening drugs for treating these diseases.
                                                                                                                         Zlotnik
                                                                                                                                      Afar D,
                                                                                                                                                                                                                                           20-SEP-2001;
13-NOV-2001;
                                                                                                                                                                                                                                                                           17-SEP-2001;
                                                                                                                                                                                                                                                                                                       17-SEP-2002; 2002WO-US029560.
                                                                                                                                                                                                                                                                                                                                       27-MAR-2003.
                                                                                                                                                                                                                                                                                                                                                                   WO2003025138-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cancer related protein SEQ ID NO:208.
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                                                                          2003-354600/33.
DB; ACC72672.
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                                                                                                                                                                                               ; 2001US-0323887P.
; 2001US-0350666P.
; 2002US-0355145P.
; 2002US-0355257P.
; 2002US-0372246P.
                                                                                                                                                                  BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis; screening; modulator;
atherosclerosis; endometriosis.
                                                                                                                                      Gish KC,
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Pred. No. 6.8e-83;
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                                                                                                                                      Mack DH,
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                                                                                                                                                                                                                                                                                                                                                                                                                                            leukaemia; ischaemia;
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                                                                                                                                      Wilson
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                                            16-MAR-2001; 2001US-0276305P
                                                                                                                                        26-SEP-2002.
                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human REG-like protein (RELP)
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                                                                                         14-MAR-2002; 2002WO-US007945
                                                                                                                                                                                     WO200274916-A2
                                                                                                                                                                                                                                                                                                 Peptide
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27. .158
/label= RELP
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Pred. No. 6.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID
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Matches 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated REG-like protein (RELP) human immunoglobulin derived protein or specified portion or variant, useful for preventing or treating a RELP protein mediated condition or malignant condition, e.g. cancer.
                                                                                                                                                                                                                                                                                             Sequence 158 AA;
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N-PSDB; ABZ21635.
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mes 158; Conserv
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Q9D858
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Q8NER7
Q8NER7
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Q8NER6
Q8NER6
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LECG_CROAT
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Q9BYZ8
                 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Al Klausner R.D., Collins F.S., Wagner L., Schemmen C.M., Schuler G.D.,

Al Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heich F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

A Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carminci P., Prange C.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gunaratne P.H.,

A Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Villalon D.K., Muzny D.M., Sodenton A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J.D., Dickson M.C.,

A Nones S.J., Marra M.A.,

Jones J. Jones J.,

Jones J
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Q9BYZ8;
01-JUN-2001
01-JUN-2001
25-OCT-2004
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MEDILINE=21210973; PubMed=11311942; DOI=10.1016/S0167-4781(00)00284-0;

Hartupee J.C., Zhang H., Bonaldo M.F., Soares M.B., Dieckgraefe B.K.;

"Isolation and characterization of a cDNA encoding a novel member of
the human regenerating protein family: Reg IV(1).";

Biochim. Biophys. Acta 1518:287-293(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Regenerating gene type IV precursor (REG-like protein) (Regenerating islet-defived family, member 4) (Gastrointestinal secretory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Kamarainen M., Heiskala
Submitted (JUN-2002) to
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Violette S., Festor E.,
Lacasa M., Lesuffleur T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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TISSUE=Colon;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2001)
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Generation and initial analysis of more than 15,000 full-length humar
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EMBL/GenBank/DDBJ databases.
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Q6X5S3
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Q6x5s4
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4 echis carin
1 homo sapien
8 pleurodeles
5 bitis gabon
8 apkistrodon
8 apkistrodon
1 homo sapien
3 echis pyram
7 echis ocell
9 echis carin
1 bitis ariet
0 echis multi
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EMBL; AF345934, AAK59869.1;
EMBL; AY126670; AAM95598.1;
EMBL; BC017089; AAH17089.1;
EMBL; AF254415; AAK48435.1;
HSSP; P22030; IIJK.
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SIGNAL
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Small intestine;
STRAIN=C57BL/6J; PubMed=11217851; DOI=J
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Q9D8G5;
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GO; GO:0005529; F:sugar binding; IE
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                   Carninci P., Hayashizaki Y.;
"High-efficiency full-length c
Meth. Enzymol. 303:19-44(1999)
                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                      full insert sequence
                                                                                                                                                                                                                                                                                                                                                                           Mus musculus adult male enriched library, clone:
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25-OCT-2004 (TrEMBLrel.
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                  MEDLINE=99279253; PubMed=10349636;
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c. Natl. Acad. Sci. U.S.A.
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                                                                                                                                                                                     FROM N.A.
57BL/6J; TISSUE=Small intestine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGNGAHLAS ILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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BLrel. 28, Last annotation update)
t male small intestine cDNA, RIKEN full-length
clone:2010002L15 product:REGENERATING GENE TY
nce (Reg4 protein).
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C_TYPE_LECTIN_2; 1.
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Rodentia;
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Pred. No. 2.5e-78;
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Sciurognathi;
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                                                                                                                       cloning.";
                     DOI=10.1038/35055500;
                                                                                                                                                                  DOI=10.1016/S0076-6879(99)03004-9;
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thi; Muridae;
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MEDLINE-2238957; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RKlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RKlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,

RA Altschell S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA History M., Salska U., Smallus D.E., Schnerch A., Schein J.E.,

RA Kores G. T. Mayra M. A.,

RA Kraywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

RA Kores G. T. Mayra M. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H., Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M. Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Kato H., Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H., Ikawa J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C., Kato Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M. Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K. Sano H., Sasaki D., Shibata Y., Shinagawa A., Shiraki T. Sogabe Y., Suzuki H., Tagami M., Tagama Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino Muramatsu M., Hayashizaki Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6J; TISSUB-Small intestine;

MEDLINB-20530913; PubMed=11076861; DOI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

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Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the RIKEN Genome Exploration Research Group "Analysis of the mouse transcriptome based c 60,770 full-length cDNAs.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=FVB/N;
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STRAIN=C57BL/6J; TISSUB=Small intestine;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
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                  "Generation and and mouse cDNA s
                                                                 Jones S.J., Marra M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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/B/N; TISSUE=Colon;
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                     cDNA sequences."
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on functional annotation
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                                            full-length human
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Scheetz T.E.,
Prange C.,
Mullahy S.J.,
Inaratne P.H.,
J., Hulyk S.W.,
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RESULT 3

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Q9D858;
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus adult male small intestine cDNA, RIKEN full-length
enriched library, clone:2010204KZ1 product:REGENERATING GENE TYE
full insert sequence.
                             SEQUENCE FROM N.A.
STRAIN-C57BL/6J, TISSUE-Small intestine;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group
"Analysis of the mouse transcriptome based o
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
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MEDLINE=21085660; PubMed=11217851;
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MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria;
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SMART; SM00034; CLECT; 1.
PROSTITE; PS50041; C. TYPE LECTIN 2; 1.
SEQUENCE 157 AA; 18398 MW; F3981722BBD83968 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GO; GO:0005615; C:extracellular space; InterPro; IPR001304; Lectin C. InterPro; IPR001390; Pancreatis_ac. Pfam; PF00059; Lectin_C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AK008049; BAB25429.1;
EMBL; BC019465; AAH19465.1;
HSSP; Q06141; 1UV0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
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STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                     RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=Reg4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:1914959; Reg4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RTKSEARHCAEMNPKDKFLTWNKNGCANRQHFLCKYK 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Small intestine;
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Rodentia;
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Pred. No. 4.8e-51;
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                    cDNA collection.";
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Murinae; Mus
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                                                                                                                                                  Team;
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RESULT 4
Q68AX7
ID Q68A
AC Q68A
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RC Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,

RA Adachi J., Aizawa K., Akahira S., Pukunishi Y., Furuno M.,

RA Arakawa T., Bono H., Carninci P., Pukuda S., Fukunishi Y., Furuno M.,

RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,

RA Hanagaki T., Hara A., Hayatsu N., Izawa M., Kasukawa T., Kato H.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

RA Kawai Y., Miyazaki A., Nabin K., Nomura K., Numazaki R., Ohno M.,

RA Mateuyama T., Miyazaki A., Nabin K., Nomura K., Numazaki T., Sakai T.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai T.,

RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai T.,

RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,

RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,

RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,

Muramatsu M., Hayashizaki Y.,

RA MILL, AKOO8438, BAB55669.1; -.

RMEL, AKOO8438, BAB55669.1; -.
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Best Local S
Matches 103
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MEDLINE=20530913, PubMed=11076861, DÖI=10.1101/gr.152600;

MEDLINE=20530913, PubMed=11076861, DÖI=10.1101/gr.152600;

Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Yokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashitzaki Y.;

"RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer.";

Genome Res. 10:1757-1771(2000).
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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STRAIN=C57BL/60; TISSUE=Small intestine;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., It
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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157 AA; 18474 MW; FD96F36CFB989368 CRC64;
                                                                                                                                                                                                                                                                                                                                  RTKSEARHCAEMNPKDKFLTWNKNGCANRQHFLCKYK 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                               YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                                                                                                                                                                                                                                                                                                                                               KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYR 157
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Pred. No. 1.9e-50;
5; Mismatches 28;
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Q68AX7; Q68AX7; 25-OCT-2004 25-OCT-2004 25-OCT-2004

(TrEMBLrel. (TrEMBLrel. (TrEMBLrel.

28,

Created)
Last sequence update)
Last annotation update)

PRELIMINARY;

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QANEAT 1D QANEAT 1D QANEAT 1D QANEAT 1D QANE DT 01-0 DT 02 Rag-0 OC Mammo OC WAmmo OX WOELL RN [1] RN KAma RL Subm DR EMBL DR HSSP DR GO; DR Inte DR HSSP DR
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                                                                                                                                                                                                                                                                                                                                EMBL; AY126671; AAM95599.1; -.
HSSP; P21963; JJZN.
HSSP; P21963; F:sugar binding; IE
GoterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
Pfam; PP00059; Lectin C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
                                                                                                                                                                                                                    PRINTS; PR01504; PNCREATITSAP.

SMART; SM00034; CLECT; 1.

PROSITE; RS50041; C TYPE LECTIN 2; 1.

SEQUENCE 113 AA; 12832 MW; AZE9DF1A729C78DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kamarainen M., Heiskala K., Submitted (JUN-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REG-like protein splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8NER7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8NER7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PF00059; Lectin_C; 1.
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EMBL; AB164049; BAD38673.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Namikawa K., Murakami K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Wistar;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Regenerating islet-derived family member
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TaxID=9606;
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                                                                                                           101;
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157 AA; 18269 MW; 55B129FB10BA4D1D CRC64;
                                MASRSMRLLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAWYLYRSWSG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MASRSMRILLILISCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTKSEARHCTEMNPKDKFLTWNKNGCTKRQHFLCKYRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP
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MASRSMRLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Ileum;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67.6%;
                                                                                                                                62.0%;
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22, Last sequence update)
26, Last annotation update)
variant 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Mismatches
                                                                                                         1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heiskala M., Andersson L.C. EMBL/GenBank/DDBJ databases
                                                                                                      Score 544; DB 2;
Pred. No. 1.2e-45;
1; Mismatches 0
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Pred. No. 2.
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Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                        IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31;
                                                                                                           0
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                                                                                                                                                                Length
                                                                                                                                                                                                                       CRC64;
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Query Match
Best Local S
Matches 75
                                                                                                                                                             PROSITE;
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                           GO; GO:0005529; F:sugar binding;
InterPro; IPRO1304; Lectin C.
Pfam; PF00059; Lectin C; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                             Klein S., Strausberg R.;
Submitted (JUN-2003) to the
EMBL; BC053817; AAH53817.1;
HSSP; P22897; 1EGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGC64513 protein.
Xenopus laevis (African clawed frog).
                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174; Windows T. Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     initiative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic and
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Similarity
                                                                                                                              PS00615; C_TYPE_LECTIN_1; 1.
PS50041; C_TYPE_LECTIN_2; 1.
160 AA; 18330 MW; 6A5502F24689179A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acad.
Conservative
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, Last sequence up
, Last annotation :
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Score 438.5; DB 2;
Pred. No. 4.1e-35;
5; Mismatches 41;
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Best Local S
Matches 62
     "Ostrich (Struthio camelus) eggshell matrix con type lectin-like proteins Isolation, amino acipostranslational modifications.";
Biochim. Biophys. Acta 1656:41-50(2004).
-!- SUBCELIULAR LOCATION: Eggshell matrix.
-!- MASS SPECTROMETRY: NWALIS343.2; MW_ERR=4; ME-RANGE-1132; NOTE-Ref.1.
-!- SIMILARITY: Contains 1 C-type lectin family InterPro; IPR003253; AntifreeZeII.
InterPro; IPR003390; Pancreatis—ac.
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
11-OCT-2002 (TrEMBLrel. 22, Last annotation update)
REG-like protein splice variant 2.
Homo sapiens (Human).
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                                                                                                                                                                                                                         SEQUENCE, SUBCELLULAR LOCATION, AND MASS SPECTROME
TISSUE-Eggshell matrix;
PubMed=14726203, DOI=10.1016/j.bbapap.2003.09.006;
Mann K., Siedler F.;
                                                                                                                                                                                                                                                                                                                                                                                                 Struthiocalcin-1 (SCA-1).
Struthio camelus (Ostrich).
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                            Archosauria; Aves;
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(Rel. 44, Last sequence update)
(Rel. 44, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                            ; Chordata; Craniata; Vertebrata; Palaeognathae; Struthioniformee;
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Primates; Catarrhini; Hominidae; Homo.
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EMBL/GenBank/DDBJ databases.
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Pred. No. 2.6
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Struthionidae;
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TISSUE-Eggshell matrix;

MEDLINE-22439773; PubMed=12431998; DOI=10.1074/jbc.M201518200;
Lakshminarayanan R., Vallyaveettil S., Rao V.S., Kini R.M.;
"Purification, characterization, and in vitro mineralization so
of a novel goose eggshell matrix protein, ansocalcin.";

J. Biol. Chem. 278:2928-2936(2003).

-i- FUNCTION: Induces spherical aggregates of calcite crystals
vitro. Believed to play an active role in the eggshell
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Direct protein sequencing; Lectin.
DOMAIN
1 132 C-type lectin.
DISULFID 3 14 By similarity.
                                                                                              Pfam, PP00059; Lectin C; 1.
PRINTS; PR00356; ANTIFRESZEII.
PRINTS; PRO1504; PKCREATITSAP.
SMART; SM00034; CLECT; 1.
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PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
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                                                                                                                                                                                                                                                                                              -!- MASS SPECTROMETRY: MW=15342; METHOD=Electrospray; RANGE=1-132
                                                                                                                                                                                                                                                        SIMILARITY: Contains 1 C-type
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                                                                                                                                                                         IPR002353; AntifreezeII.
IPR001304; Lectin_C.
IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION, SUBUNIT,
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(Rel. 41, Last seq
(Rel. 44, Last ann
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44, Last annotation update)
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Pred. No. 1.1
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                                                                                                                                      RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RP SEQUENCE FROM N.A.

RESTRAIN=C57BL/6J; TISSUE=Thymus;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.24260389;

RX MEDLINE=2388257; DOI=10.1073/pnas.24260389;

RX MEDLINE=2388257; DOI=10.1073/pnas.24260389;

RX MEDLINE=2388257; DOI=10.1073/pnas.24260389;

RX MEDLINE=2388257; DOI=10.1073/pnas.2426032;

RX MEDLINE=2388257; DOI=10.10
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P43137;
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01-NOV-1995
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DISULFID
SEQUENCE
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05-JUL-2004 (Rel. 44, Last annotation update)
Lithostathine 1 precursor (Pancreatic stone protein 1) (PSP)
(Pancreatic thread protein 1) (PTP) (Islet of langerhans reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=C57BL/6J; PubMed=8340418;
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                     Proc.
                                                                                                                            and mouse cDNA sequences.";
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RESULT 11
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Best Local S
Matches 52
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InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PF00059; Lectin_C; 1.
PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR00356; ANTIFREEZEII.
PRINTS; PR01504; PRCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN_2; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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                                                                                                                01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Lithostathine precursor (Pancreatic stone protein) (PSP) (Pancreatic thread protein) (PTP) (Islet of langerhans regenerating protein) (REC (Islet cells regeneration factor) (ICRF).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
         SEQUENCE FROM N.A.
MEDLINE=91093273; PubMed=1985964;
                                               NCBI_TaxID=10116;
                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                       Name=Reg1; Synonyms=Reg;
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D14010; BAA03111.1; -.
                                                                                           Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; A47148; A47148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed strongly in pancreas, weakly in liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          normal exocrine pancreas, but not in normal pancreatic isle
Expressed strongly in pancreas, moderately in gallbladder,
                                                                                                                                                                                                                  RAT
                                                                                                                                                                                                                                                                                   118
                                                                                                                                                                                                                                                                                                           113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC028761; AAH28761.1;
                                                                                                                                                                                                                                                                                                                                     60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P05451; 1LIT
                                                                                                                                                                                                                                                                                                                                                                                                                  10 LILSCLAKTGVLGDIIMRP------SCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                         æ
                                                                                                                                                                                                                                                                                                                                                                                                                                             | Similarity
| 52; | Conser
                                                                                                                                                                                                                                                                                                ELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWIDGAM 112
                                                                                                                                                                                                                                                                                   FLYKSWATGSPNSSNRGYCVSLTSNTGYKKWKDDNCDAQYSFVCKFK
                                                                                                                                                                                                                                                                                                                                                                                         ILLSCL----IVLSPSQGQEAEEDLPSARISCPEGSNAYSSYCYYFTEDRLTWADA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B,
                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
161
153
129
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165
163
                                                                 Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18518
                                                                                                                                                                                                                                                                                                                                                                                                                                                         29.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               By similarity.
Lithostathine 1.
C-type lectin.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlCNMac...
W; 2950174AF5D666BA (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 254.5;
Pred. No. 5.2
                                                                 Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                  165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.2e-17;
                                                                 Vertebrata;
thi; Muridae;
                                                                                                                                                                                                                  ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                              51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 165;
                                                                 Euteleostomi;
Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Potential)
                                                                                                                                                                                                                                                                                   164
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                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                  Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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s.,

Verdier J.M.,

Iovanna

<u>ر</u> :

Dagorn J.-C., Giorgi D.;

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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                         EMBL; L07512; AAA41533.1; -.
EMBL; M62930; AAA41974.1; -.
EMBL; M18962; AAA42028.1; -.
EMBL; D26164; BAA05149.1; -.
PIR; A28351; A28351.
HSSP; P05451; ILIT.
                                        DISULFID
CARBOHYD
SEQUENCE
                                                                                DOMAIN
DISULFID
DISULFID
                                                                                                                                      Direct
SIGNAL
                                                                                                                                              PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Direct protein sequencing; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=90031455; PubMed=2680252;
Adrich Z., de Caro A.M., Guidoni A.A., Woudstra M.E., R
"Characterization in rat pancreatic juice of a protein
the human pancreatic stone protein.";
Comp. Biochem. Physiol. 93B:793-797(1989).
-i- FUNCTION: Might act as an inhibitor of spontaneous
carbonate precipitation.
-i- TISSUE SPECIFICITY: Expressed only in regenerating
                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restude by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93326645; PubMed=7916640; DOI=10.1016/0167-4781(93)90100-R; Dusetti N.J., Frigerio J.M., Dagorn J.-C., Iovanna J.L.; "Rapid PCR cloning and sequence determination of the rat lithostath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Terazono K., Yamamoto H., Takasawa S., S
Tochino Y., Okamoto H.;
Tochino Y., Okamoto H.;
"A novel gene activated in regenerating
J. Biol. Chem. 263:2111-2114(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Rat pancreatic stone protein messenger RNA. Abundant expression in mature exocrine cells, regulation by food content, and sequence identity with the endocrine reg transcript.";

J. Biol. Chem. 266:786-791(1991).
                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Miyashita H., Suzuki Y., Watanat
Yonekura H., Okamoto H.;
"Structure and characterization
Seikagaku 65:1082-1082(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=88115343; PubMed=2963000; Terazono K., Yamamoto H., Takasawa
                                                                                                                                                                                                                     InterPro; IPRO01304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
Pfam; PF00059; Lectin_C; 1.
                                                                                                                                                                                                                                                            RGD; 3552; Reg1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΓISSUE≔Pancreas;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1174:99-102(1993)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in normal pancreatic islets, insulinomas or regenerating SIMILARITY: Contains 1 C-type lectin family domain.
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33
35
63
136
129
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Okamoto H.;
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                                                      163
163
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161
153
129
                                         18672 MW;
 30
 . 6%;
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                                      C-type lectin.
By similarity.
By similarity.
By similarity.
By similarity.
N-linked (GlcNAc...
W; 9B61EB236B82CF8A C
Score
Pred.
                                                                                                                        Lithostathine.
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254.5; DB 1;
No. 5.2e-17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shiga K., Yonemura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            islets.";
                                                                                                                                                  Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the rat lithostathine
                                           CRC64;
                                                                                                                                                  Signal.
            Length
                                                      (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rovery M.;
n homologous
                                                                                                                                                                                                                                                                                                                                                                                                                              restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              islets,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           calcium
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                                                                                                                                                                                                                                                                                                                                                                                                                                            a collaboration
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STR2_STRCA
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                                                                                                                                                               문
                                                                                                                                                                                                                                                                                                                                                                                                                                              FITTING DESCRIPTION OF THE PROPERTY OF THE PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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Best Local S
Matches 48
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                        MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biochim. Biophys. Acta 1696:41-50(2004).
-!- SUBCELLULAR LOCATION: Eggshell matrix.
-!- MASS_SPECTROMETRY: MW=16834.1; MW_ERR=2; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Eggshell matrix;
PubMed=14726203; DOI=10.1016/j.bbapap.2003.09.006;
Mann K., Siedler F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Struthiocalcin-2 (SCA-2). Struthio camelus (Ostrich)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (Rel.
05-JUL-2004 (Rel.
05-JUL-2004 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00615; C_TYPE_LECTIN_1; PROSITE; PS50041; C_TYPE_LECTIN_2; Direct protein sequencing; Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO1504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Ostrich (Struthio camelus) eggshell matrix type lectin-like proteins. Isolation, amino
                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RANGE=1-142; NOTE=Ref.1.
-I- SIMILARITY: Contains 1 C-type lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AND SER-68,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8801;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Archosauria; Aves;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            posttranslational modifications.
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                        139
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                                                                                                                                                                                                                                                                              Similarity
LTWSSNECNKRQHFLCKYR
                                                                                                                                                                                                           RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID
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                                                                   OPYSDSEEEAGEEVWIGLHRPLGRRNWEWSDGTKLDYGSWYRDVFLRRRACVALEDTTDF
                                                                                                                                                               RAGCAKGWIPFDGRCYGFFPQELSWRRAEGFCQRLGARTHLASIHSEEEHQAIVSMLASS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION, PHOSPHORYLATION SITES B, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                             68
142
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                                                                                                                                                                                                                                                                                                                                                                                           134
662
662
                                                                                                                                                                                                                                                        Conservative
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44, Last sequence update)
44, Last annotation update)
                                                                                                                 RSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKSMGGNKHCAEMSSNNNF 138
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138
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                                                                                                                                                                                                                                                                            28.1%;
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                                                                                                                                                                                                                                                                                                                                             By similarity.
By similarity.
By similarity.
By similarity.
Phosphoserine.
Phosphoserine.
Phosphoserine.
Phosphoserine.
                                                                                                                                                                                                                                                                            Score 247; DB 1;
Pred. No. 2.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          c-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; hae; Struthioniformes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    acid sequence,
                                                                                                                                                                                                                                                        66;
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                                                                                                                                                                                                                                                                                                                                                  CRC64;
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                                                                                                                                                                                                                                                        Indels
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Struthionidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SER-62; SER-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29;
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01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
05-JUL-2004 (Rel. 4
                                                                                                                                                                            DISULFID
DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D63361; BAA18930.1
EMBL; D63362; BAA18931.1
HSSP; P05451; 1LIT.
MGD; MGI:109406; Reg3g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-C57BL/60; TISSUE-Liver, and Pancreas;
STRAIN-C57BL/60; TISSUE-Liver, and Pancreas;
MEDLINE-97208868; PubMed-9055810; DOI-10.1016/S0378-1119(96)00589-6;
Narushima Y., Unno M., Nakagawara K.-I., Mori M., Miyashita H.,
Suzuki Y., Noguchi N., Takasawa S., Kumagai T., Yonekura H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Structure, chromosomal localization and expression of mouse genes encoding type III Reg, RegIII alpha, RegIII beta, RegIII gamma."; Gene 185:159-168(1997).
                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                              SMART; SM00034; CLECT; 1.

PROSITE; PS00615; C_TYPE_LECTIN_1; FA

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=Pap3; Synonyms=Reg3g;
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUL-2004 (Rel. 44, Last annotation update)
Pancreatitis-associated protein 3 precursor (REG III-gamma)
                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                   Acute phase;
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; Lectin_C; 1.
PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Okamoto H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Might be a stress protein bacterial proliferation. SUBCELLULAR LOCATION: Secreted. TISSUE SPECIFICITY: Constitutively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               healthy pancreas. SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               intestine, moderately in colon and
                                                         13
                                                                                       10
73
                          63
                                                                                                                                  Similarity
SG-HLVSVLSGAEASFLSSMIKSSGNSGQYVWIGLHDPTLGYEPNRGGWEWSNADVMNYI
                        NGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDP-----QKRQQWQWIDGAMYLYR
                                                       MILISCLMLLSQVQGEVAKKDAPSSRSSCPKGSRAYGSYCYALFSVSKNWYDADMACQKRP
                                                                                   LLLSCL-AKTGVLGDII-----MRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG
                                                                                                                                                                            145
174 AA;
                                                                                                                   Conservative
                                                                                                                                                                                                          27
38
40
68
                                                                                                                                                                                                                                                                                 Inflammatory
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174
174
174
170
170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      be a stress protein involved in the control of
                                                                                                                                                                              19307 MW;
                                                                                                                                 28.1%;
35.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update
                                                                                                                                                                                                                                                                   response; Lectin; Multigene family; Signal. Potential.
                                                                                                                   24;
                                                                                                                                                                                       Pancreatitis-associated protein 3.
C-type lectin.
By similarity.
By similarity.
By similarity.
                                                                                                                               Score 246.5; DB 1;
Pred. No. 3.4e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                            5575E9E56A4D8CEF CRC64;
                                                                                                                   Mismatches
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                                                                                                                                             Length
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low level
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131
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RESULT 14
Q6TRS6
ID Q6TRS
AC Q6TRS
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Q6QX33
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Best Local S
Matches 48
                                                                                                                  Q6QX33; PRELIMINARY;
Q6QX33;
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
05-JUL-2004 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning, expression, and structural analysis of recombinant c-type lectin from the Bothrops jararacussu snake venom."; protein Expr. Purif. 35:344-352(2004).

EMBL; AY388642; AAQ92957.1; -.
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR003304; Lectin C.
InterPro; IPR003304; Lectin C.
InterPro; IPR003900; Pancreatis_ac.
Pfam; PF00059; Lectin C.
Pfam; PF00059; Lectin C.
Pfam; PF00059; Lectin C.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
                                NCBI_TaxID=8723;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
CHAIN 24 157 BJcul.
             SEQUENCE FROM N.A.
                                                   Viperidae; Crotalinae;
                                                                            Eukaryota; Metazoa; Chordata; Craniata;
                                                                                          Bothrops insularis (Island
                                                                                                       C-type lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kassab B.H., de Carvalho D.D.,
Pereira G.A., Novello J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=15135412; DOI=10.1016/j.pep.2004.02.012;
Kassab B.H., de Carvalho D.D., Oliveira M.A., B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel.
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05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q6TRS6
TISSUE=Venom gland
                                                                Lepidosauria; Squamata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lepidosauria; Squamata; Sclerogl
Viperidae; Crotalinae; Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bothrops jararacussu
                                                                                                                                                                                                                                           145 VCESKNAFLC
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                                                                                                                                                                                                                                                                                                                                                                             29
                                                                                                                                                                                                                                                                                                                                                                                                        48;
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                                                                                                                                                                                                                                                                                              GOSEVWIGLCDKKKDFSWEWTDRSCTDYLSWDKNQPDHYQNKEFCVELVSNTGYRLWNDQ
                                                                                                                                                                                                                                                                                                                     SQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKS---MGGNKHCAEMSSNNNFLTWSSN 144
                                                                                                                                                                                                                                                                                                                                                                  SCAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYISGYQR
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llarity 36.9%;
Conservative 1
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                                                   Bothrops
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27,
27,
                                                                Scleroglossa;
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                                                                              jararaca) (Queimada jararaca)
ta; Craniata; Vertebrata; Eute
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Last
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Last sequence up
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Pred. No. 4.5e-16;
6; Mismatches 62
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                                                                                                                     annotation
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                                                                                                                                 sequence
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                                                                  Serpentes;
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on update)
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                                                                    Colubroidea;
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                                                                              Euteleostomi;
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RA Junqueira-de-Azevedo I.L.M., Dutra D.L.S., Pujol-Luz M., Castro H.C.,

RA Ho P.L., Zingali R.B.;

RS LDMnitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.

DR GO; GO:005529; F:sugar binding; IEA.

DR GO; GO:005529; F:sugar binding; IEA.

DR InterPro; IPR002353; AntifreezeII.

DR InterPro; IPR001304; Lectin C.

DR InterPro; IPR003990; Pancreatis_ac.

DR FARM; PR00035; ANTIFREEZEII.

DR PRINTS; PR00356; ANTIFREEZEII.

DR PRINTS; PR01504; PNCREATITSAP.

DR RNART; SM00034; CLECT; 1.

DR PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

DR PROSITE; PS00615; C_TYPE_LECTIN_2; 1.

DR PROSITE; PS00611; C_TYPE_LECTIN_2; 1.

KW Lectin.

SQ SEQUENCE 158 AA; 18636 MW; OFA6303E34967EE4 CRC64;
                                                                                                                                                                                                                                                                                                           Query Match 27.7%; Score 243.5; DB 2; Length 158; Best Local Similarity 34.0%; Pred. No. 6e-16; Matches 51; Conservative 22; Mismatches 68; Indels 9.
                                                                                                              126 NKHCAEMSSNNNFLTWSSNECNKRQHFLCK 155
                                                                           126 KEFCVÉLVSDTGYRLWNDQVCESKNAFLCQ 155
                                                                                                                                                                                                                                  66 FHLYGESPEIAEYISDYHKGQSEVWIGLWDKKKDFSWEWTDRSCTDYLSWDKNQPDHYQN 125
                                                                                                                                                                                 70 ILSLKEASTIAEYISGYQRSQ-PIWIGLHDPQKRQQWQWIDGAMYLYRSWSGKS---MGG
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 su
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Perfect score:
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Gapop 10.0 ,
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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 GenCore version Copyright (c) 1993 - 2005
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A28351
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reg II, regenerati
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                                                                                 brevican -
                                                                                               pancreatitis-assoc
                                                                               human
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RESULT 2 A28351 A28351 Pancreatic stone protein precursor - rat N;Alternate names: lithostathine C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Mar-1990 #sequence revision 31- C;Accession: A28351; A39081; PL0147; S3461- R;Terazono, K.; Yamamoto, H.; Takasawa, S. J. Biol. Chem. 263, 2111-2114, 1988 A;Title: A novel gene activated in regener A;Reference number: A92704; MUID:88115343; A;Accession: A28351 A;Accession: A28351 A;Accession: A28351 A;Accession: A28351	RESULT 1 A47148 reg I, regenerating isl C;Species: Mus musculus C;Species: Mus musculus C;Accession: A47148 R;Unno, M.; Yonekura, I J. Biol. Chem. 266, 155 A;Title: Structure, ch A;Reference number: A4714 A;Reference number: A4714 A;Residues: preliminary A;Molecule type: DNA A;Residues: 1-165 CUNN; A;Cross-references: UNI C;Genetics: 21/1; 60/3; C;Superfamily: tetranec F;35-161/Domain: C-type F;35-46,63-161,136-153) Query Match Best Local Similarity Matches 52; Conser Qy 10 LLLSCLACT Oy 55 ELECOSYMNS Qy 113 YLYRSW-SC Qy 113 YLYRSW-SC Qy 111 FLYKSWATC		
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ic stc ate na 3: Rat 3: Rat lon: A lon, K. Chem. A now nce nu lon: A	SULT 1 7148 7148 Species: Mus musculus (house mouse) Date: 03-May-1994 #sequence_revision Accession: A47148 Biol. Chem. 268, 15974-15982, 1993 Title: Structure, chromopomal localiz: Reference number: A47148; MUID:933402 Accession: A47148 Status: preliminary Molecule type: DNA Residues: 1-165' <unn> Cross-references: UNIPROT:P43137; GB:Introns: 21/1; 60/3; 10/3; 144/1 Introns: 21/1; 60/3; 106/3; 144/1 Superfamily: tetranectin; C-type lect: 35-161'/Domain: C-type lectin homology 35-46,63-161,136-153/Disulfide bonds: Coury Match Best Local Similarity 31.1%; Pred. Matches 52; Conservative 35; Mid Matches 52; Conservative 35; Mid Matches 52; Conservative 35; Mid 10 LLLSCLAKTGVLGDIIMRP 11 SILECQSYGNGAHLASILSLKEASTI: 16 DLFCQNMNSG-YLVSVLSQAEGNEV 113 YLYRSW-SGKSMGGNK-HCAEMSSNI 118 FLYKSWATGSPNSSNRGYCVSLTSN</unn>		185 184.5 182.5 182.5 181.5 181.7 181 179 179 179 177.5 177.5 177.5
ne pr mes: tus n -1990 28351 ; Yam ; Yam el ge el ge el ge el ge el ge mber:	rating isls musculus y-194 #se A47148 A47148 Onekura, H. 1. 268 157 A47148 Pe: DNA Pe:		190000000000000000000000000000000000000
otein litho lorveg #seq ; A39 amoto 2111 ne ac A927 NA	ng isle seculus 94 #seq 48 1597 e, chrc r: A471 A471 DNA DNA DNA DNA C-type 6-153/D C-type 6-153/D C-coserv Conserv Conserv Conserv Conserv Conserv Conserv Conserv Conserv Conserv		HHOBF 66444 W 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
i prec icus icus uence 081; H.; 2114 tivat	merating islet cells - mou May-1994 #sequence_revision 1. A47186 Yonekura, H.; Nakagawara, lem. 268, 15974-15982, 1992 Yonekura, H.; Nakagawara, lem. 268, 15974-15982, 1993 Yonekura, H.; Nakagawara, lem. 268, 15974-15982, 1993 Yonekura, H.; Nakagawara, lem. 268, 15974-15982, 1993 Yonekura, H.; Nakagawara, lem. 168, 15974-16982, 1993 lem. 16974, 10673; MUID:9334 lem. 16973; 10673; 144/1 ly: tetranectin; C-type lem. 161,136-153/Disulfide bond long. 161,136-153/Disu		883 1257 146 301 147 291 291 291 291 291 2409 311 162 162 162 162 162 162 162
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coursor - rat hine (Norway rat) e revision 31-Mar-1990 PD1017; S34618; FTAL83awa, S.; Shiga, 4, 1988 ted in regenerating is ted in regenerating is	ating islet cells - mouse [musculus (house mouse) 47148 nekura, H.; Nakagawara, K.; Watanabe, T.; Miyashita, H.; Mor 268, 15974-15982, 1993 ture, Chromopomal localization, and expression of mouse reg iminary initiary ne: DNA 165'-CUNN nices: UNIPROT:P43137; GB:D14010; NID:B340418 165'-CUNN nices: UNIPROT:P43137; GB:D14010; NID:B391771; PIDN:BAA03111. 1; 60/3; 106/3; 144/1 tetranectin; C-type lectin homology n: C-type lectin homology <lch #status="" 165;="" 254.5;="" 29.0%;="" 29;="" 2;="" 31.1%;="" 35;="" 51;="" 9.2e-18;="" bonds:="" conservative="" db="" disulfide="" gaps="" imilarity="" indels="" length="" lllsclaktgvlgdiimrp<="" lllsclaktgvlgdiimrpscapgwfyhksncygyerklrnwsda="" mismatches="" nils-153="" no.="" pred.="" predicted="" score="" td="" =""><td>Ą</td><td>\$49126 \$727135 \$13165 \$13165 \$13165 \$13167 \$</td></lch>	Ą	\$49126 \$727135 \$13165 \$13165 \$13165 \$13167 \$
a - 60.3x	DOUSE 100 83-May-1994 a, K.; Watanabe 93 340209; PMID:83 1ectin homology 1core 254.5; DB red. No. 9.2e-1 Mismatches SQEAEEDLPSARISC GQEAEEDLPSARISC GGETVASLIKESGTTD MSSNNNFLTWSSNEC :: GMFVASLIKESGTTD MSSNNNFLTWSSNEC ::	ALIGNMENTS	
ar-1990 #tex Shiga, K.; Shiga islets. PMID:2963000	7-May-1994; Watanabe, tion, and e 9; PMID:834 14010; NID: 14010; NID: 14010; NID: 254.5; DB 48tatus pre 254.5; DB matches 5SCA EDLPSARISCP EDLPSARISCP EYI-SGYORS	STN	
6 🗗	y-1994 #text_change 09-Jul-200 tanabe, T.; Miyashita, H.; Mor , and expression of mouse reg; MID:8340418 0; NID:9391771; PIDN:BAA03111. mology tus predicted tus predicted 5; DB 2; Length 165; 9.2e-18; hes 51; Indels 29; Gaps hes 51; Indels 29; GapsSCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSDASCAPGWFYHKSNCYGYFRKLRNWSSGSL SARISCPHUIGLHDPKRNRRWHWSSGSL WSSNECNKRQHFICKYR 157		
#text_c K.; Yon ets.	#text_c T:, Mi T:, Mi O418 0418 0418 0418 0418 0418 0418 0418 0		
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C;Accession: S78596
R;Baernholdt, D.; Andersen,
submitted to the Protein Sec
                                                                                                                                                                                                                                                                                                                          C;Species: Gallus gallus (chicken)
C;Date: 24-Oct-1998 #sequence_revision
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S78596
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-165 <DUS>
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A;Residues: 22-69 <ADR>
A;Residues: 22-69 <ADR>
A;Experimental source: pancreas
A;Experimental source: pancreas
R;Dusetti, N.J.; Frigerio, J.M.; Dagorn, J.C.; Iovanna, J.L.
Biochim. Biophys. Acta 1174, 99-102, 1993
Biochim. Biophys. Acta 1174, 99-102, 1993
A;Tille: Rapid PCR cloning and sequence determination of the rat lithostathine
A;Reference number: S34618; MUID:93326645; PMID:7916640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GB:M62930; GB:J05722; NID:g206462; PIDN:AAA41974.1; PID:g206463 R;Adrich, Z.; De Caro, A.M.; Guidoni, A.A.; Woudstra, M.E.; Rovery, M. Comp. Biochem. Physiol. B 93, 793-797, 189. Comp. Biochem. Physiol. B 93, 793-797, 191. Comp. Biochem. Physiol. B 93, 793-797, 191. Comp. Raracterization in rat pancreatic juice of a protein homologous to the human A;Reference number: PL0147; MUID:90031455; PMID:2680252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:P10758; GB:M18962; NID:g206604; PIDN:AAA42028.1; R;Rouquier, S.; Verdier, J.M.; Iovanna, J.; Dagorn, J.C.; Giorgi, D. J. Biol. Chem. 266, 786-791, 1991
                                                                                    A; Experimental source: egg-shell C; Superfamily: tetranectin; C-ty
                                                                                                                                            A; Molecule type: protein A; Residues: 1-142 < BAE>
                                                                                                                                                                                            A; Reference number: S78596
A; Accession: S78596
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A; Residues: 1-165 < ROU>
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A;Accession: A39081
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                                                             C; Keywords:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords: pyroglutamic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;22-165/Product: pancreatic stone protein #status predicted <MAT>;35-161/Domain: C-type lectin homology <LCH>;22/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form)
        ;61,67/Binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
'itamily: ....

ords: phosphoprotein

33-138,113-130/Disulfide bonds:

hosphate (Ser) (
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                                                                                                                                                                                                                                                                                                                                                                                           chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SDAELECQSYGNGAHLASILSLKEASTIAEYI -- SGYQRSQPIWIGLHDPQKRQQWQWID 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKWRDNSCDAQLSFVCKFK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEADLFCQNMNSG-YLVSVLSQAEGNFLASLIKESGTTAAN-VWIGLHDPKNNRRWHWSS
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                                                                                                                                                                                                                                              Sequence
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                                                                                 C-type lectin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38;
                                                                                                                                                                                                                                                 Database, September 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
        (covalent)
                              #status experimental
                                                                                                                                                                                                                                                                                                                             24-Oct-1998 #text_change 20-Sep-1999
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     #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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A;Gene: GDB:REG1B; REG1
A;Cross-references: GJB:342079
A;Cross-references: GJB:342079
A;Map position: 2p12-2p12
A;Introns: 22/1; 61/3; 107/3; 145/1
A;Introns: 22/1; 61/3; 107/3; 145/1
C;Superfamily: tetranectin; C-type lectin homology
C;Reywords: glycoprotein; lectin; panoreas; pyroglutamic acid
F;1-22/Domain: signal sequence #status predicted <SIG>F;1-22/Domain: signal sequence #status predicted <SIG>F;23-166/Product: regenerating islet lectin lbeta #status predicted
F;34-166/Product: pancreatic stone protein #status predicted <MAT2>
F;36-162/Domain: C-type lectin homology <CCH>A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Molecule type: DNA
A;Residues: 1-166 <BAR>
A;Residues: UNIPROT:P48304; GB:L08010; NID:g307368; PIDN:AAA18204.1; PID:g487726
A;Note: this gene appears to be expressed in pancreas and liver
R;Moriizumi, S.; Watanabe, T.; Unno, M.; Nakagawara, K.; Suzuki, Y.; Miyashita, H.; Yone
Biochim. Biophys. Acta 1217, 199-202, 1994
A;Title: Isolation, structural determination and expression of a novel reg gene, human r.
A;Reference number: S42729; MUID:94153997; PMID:8110835
A;Accession: S42729
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RGHU1B
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A;Cross-references: GB:D17291; NID:g474307; PIDN:BAA04124.1; PID:g474308
C;Comment: This protein is found in pancreatic calculi of mammals. The ti
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: A gene homologous to the reg gene is expressed A;Reference number: S34591; MUID:93351647; PMID:8348956 A;Accession: S34591
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence revision 03-Aug-1995 #text_change
C;Accession: S34591; S42729; A44712
R;Bartoli, C.; Gharib, B.; Giorgi, D.; Sansonetti, A.; Dagorn, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regenerating islet lectin 1-beta precursor - human N;Alternate names: reg-related protein; reg1-beta protein N;Contains: pancreatic stone protein (PSP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
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                                                                                                                                                                                                                                      F;36-47,64-162,137-154/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                              F;23/Modified site: pyrrolidone carboxylic acid (Gln) (in mature F;27/Binding site: carbohydrate (Thr) (covalent) #status predicte F;33-34/Cleavage site: Arg-Ile (trypsin) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Residues: 1-166 < MOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEBS Lett. 327, 289-293, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                Local Similarity
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                                                          27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46;
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                                                                                                                    46;
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RISCPEGTNAYRSYCYYFNEDPETWYDADLYCONMNSG-NLVSVLTQAEGAFVASLIKES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DGSGEGADGRVWIGLHRPAGSRSWRWSDGTAPRFASWHRTAKARRGGR-CAALRDEEAFT 123
                                                          RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGY 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGPGWVPTPGGCLGFFSRELSWSRAESFCRRWGPGSHLAAVRSAAELRLLAELLNASRGG
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                                                                                                                    Conservative
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                                                                                                                                                   34.3%;
                                                                                                                                                                           27.3%;
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                                                                                                                 Score 240; DB 1;
Pred. No. 2.5e-16;
7; Mismatches 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 241.5; DB 2
Pred. No. 1.5e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                       57;
                                                                                                                                                                        Length 166
                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                            form) #status predicted
                                                                                                                    Gaps
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         91
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R;Suzuki, Y.; Yonekura, H.; Watanabe, T.; Unno, M.; Moriizumi, Gene 144, 315-316, 1994
A;Title: Structure and expression of a novel rat RegIII gene.
A;Reference number: I60296; MUID:94314238; PMID:8039722
A;Accession: I60296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regenerating protein III (reg III) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C;Accession: I60296; I83377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Unno, M., Yonekura, H.; Nakagawara, K.; Watanabe, T.; Miyashit J. Biol. Chem. 268, 15974-15982, 1993
A;Title: Structure, Chromosomal localization, and expression of A;Reference number: A47148; MUID:93340209; PMID:8340418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              reg II, regenerating islet cells - mouse C;Species: Mus musculus (house mouse) C;Date: 03-May-1994 #sequence_revision 03-May-1994 C;Accession: B47148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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A; Residues: 1-173 < UNN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A; Accession: B47148
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                                                                                                                                                                                              A;Accession: I83377
A;Status: preliminary; translated
A;Molecule type: DNA
A;Residues: 1-174 <RE2>
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183377
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                                                                                                                                                    A;Cross-references: GB:D26078; NID:g471159; PIDN:BAA05071.1; C;Genetics:
                                                                                                                                                                                                                                                                                     A, Cross-references:
                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-174 < RES>
                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Superfamily: tetranectin; C-type lectin homology;43-169/Domain: C-type lectin homology <LCH>;43-54,71-169,144-161/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;Genetics:
                                                             ;Introns: 25/1; 64/3; 110/3; 153/1
;Superfamily: tetranectin; C-type lectin homology
;39-170/Domain: C-type lectin homology <LCH>
                                                                                                                              Gene: RegIII
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    119 HWSSGSLFLFKSWATGAPSTANRGYCVSLTSNTAYKKWKDENCEAQYSFVCKFR 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 RLTWGEADLFCQNM-NAGHLVSILSQAESNFVASLVKESGTTASN-VWTGLHDPKSNRRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QWIDGAMYLYRSWS--GKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LRNWSDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAQNINVYLILFLCLMFLSYSQGQVAEEDFPLAEKDLPSAKINCPEGANAYGSYCYYLIED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STDDSNVWIGLHDPKKNRRWHWSSGSLVSYKSWDTGSPSSANAGYCASLTSCSGFKKWKD 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.9%; Score 236.5; DB 2 ilarity 28.7%; Pred. No. 5.8e-16; Conservative 33; Mismatches 72
                                                                                                                                                                                                                                                                                     UNIPROT: P35231; GB: D23676; NID: g471157;
26.9%;
35.3%;
Score 236.5; DB 2;
Pred. No. 5.8e-16;
                                                                                                                                                                                                                                       from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                    Length
                                                                                                                                                                                                                                                                                     PIDN:BAA04904.1; PID:g47115
                                                                                                                                                                           PID:g471160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              173;
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C;Species: Crotalus atrox (western diamondback rattlebnake)
C;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change 09-Jul-2004
C;Accession: A38609
R;Hirabayashi, J.; Kusunoki, T.; Kasai, K.
J. Biol. Chem. 266, 2320-2326, 1991
A;Title: Complete primary structure of a galactose-specific lectin from the A;Reference number: A38609; MUID:91115849; PMID:1989986
A;Accession: A38609; MUID:91115849; PMID:1989986
       A;Residues: 1-174 <DUS>
A;Residues: 1-174 <DUS>
A;Residues: 1-174 <DUS>
A;Cross-references: UNIPROT:P42854; EMBL:U09193; NID:g483931; PIDN:AAA79231.1;
A;Cross-references: UNIPROT:P42854; EMBL:U09193; NID:g483931; PIDN:AAA79231.1;
R;Frigerio, J.M.; Dusetti, N.J.; Garrido, P.; Dagorn, J.C.; Iovanna, J.L.
Biochim. Biophys. Acta 1216, 329-331, 1993
Biochim. Biophys. Acta 1216, 329-331, 1993
A;Title: The pancreatitis associated protein III (PAP III), a new member of the A;Reference number: S43438; MUID:94060113; PMID:8241280
                                                                                                                                                                  A;Title: Cloning, expression and chromosomal localization A;Reference number: S54979; MUID:95234061; PMID:7717998 A;Accession: S54979 A;Status: preliminary A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                 R;Dusetti, N.J.; Frigerio, Biochem. J. 307, 9-16, 1995
                                                                                                                                                                                                                                                                                                                                               pancreatitis-associated protein PAP-3 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 23-Aug-1995 #Bequence revision 19-Oct-1995 #text_change 09-Jul-2004
C;Accession: S54979; S43438
                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
S54979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: tetranectin; C-type lectin homology F;3-131/Domain: C-type lectin homology <LCH> F;3-14,31-131,106-123/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: protein
A;Residues: 1-135 <HIR>
A;Cross-references: UNIPROT:P21963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
A38609
A; Accession: S43438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ectin, galactose-specific - western diamondback rattlesnake
;Species: Crotalus atrox (western diamondback rattlesnake)
;Date: 23-Aug-1991 #sequence_revision 23-Aug-1991 #text_change
;Accession: A38609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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34.4%; Pred. No. 9.8e-1
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                                                                                                                                                                                                                                                                                                                          J.M.; Szpirer, C.; Dagorn, J.C.; Iovanna,
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A;Molecule type: protein
A;Residues: 38-138;141-175 <CAI>
A;Residues: 38-138;141-175 <CAI>
C;Comment: The purified protein undergoes a reversible globule-fibril transformation C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; extracellular protein; pancreas
C;Keyroduct: pancreatic thread protein chain A #status experimental <ACH>
F;38-138;Product: pancreatic thread protein chain B #status experimental <BCH>
F;141-175/Product: pancreatic thread protein chain B #status experimental <BCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P23132; GB:M59794; NID:g163648; PIDN R;Cai, L.; Harris, W.R.; Marshak, D.R.; Gross, J.; Crabb, J.W. J. Protein Chem. 9, 623-632, 1990
A;Title: Structural analysis of bovine pancreatic thread protein. A;Reference number: A53897; MUID:91197388; PMID:2085387
A;Accession: A53897
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    pancreatitis-associated C;Species: Rattus norvec
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A; Residues: 1-175 < DEL>
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                                                                                A48689
                                                                                                                        RESULT 10
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                                                                                                                                                                                                                                                                                                         114 LYRSW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKY 156
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                                                                                                                                                                                                                                     NYVAWETDPAAISSPGYCGSLSRSSGYLKWRDHNCNLNLPYVCKF
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    norvegicus
protein PAP-2 - i
gicus (Norway rat)
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regenerating islet lectin 1-alpha precursor [validated] - human
N,Alternate names: lithostathine; pancreatic thread protein (PTP); reg I pround in the protein stone protein (PSP)
C.Species: Homo sapiens (man)
C.Date: 31-Mar-1990 #sequence revision 03-Aug-1995 #text_change 09-Jul-2004
C;Accession: A35197; B23351; S12950; S02767; S02419; S00713; S01471; A25246
R;Watanabe, T.; Yonekura, H.; Terazono, K.; Yamamoto, H.; Okamoto, H.
J. Biol. Chem. 265, 7432-7439, 1990
A.Title: Complete nucleotide sequence of human reg gene and its expression in product of the gene.
A;Reference number: A35197; MUID:90237042; PMID:2332435
A;Accession: A35197.
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                                                         A;Note: sequence determined from protein isolated after human cDNA sequence was cloned R;de Caro, A.M.; Adrich, Z.; Fournet, B.; Capon, C.; Bonicel, J.J.; de Caro, J.D.; Rove Biochim. Biophys. Acta 994, 281-284, 1989
B;Title: N-terminal sequence extension in the glycosylated forms of human pancreatic st A;Reference number: S02767; MUID:89150292; PMID:2493268
A;Accession: S02767
                                                                                                                                                                                                                                                                                                                                      FEBS Lett. 272, 85-88, 1990
A;Title: Isolation and characterization of
A;Reference number: S12950; MUID:91032149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Terazono, K.; Yamamoto, H.; Takasawa, S.; Shiga, K.; J. Biol. Chem. 263, 2111-2114, 1988
A;Title: A novel gene activated in regenerating islets. A;Reference number: A92704; MUID:88115343; PMID:2963000
A;Accession: B28351
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-174 <FRI>
A;Residues: 1-174 <FRI>
A;Cross-references: UNIPROT:P35231; GB:L10229; NID:g409014; PIDN:AAA02980.1; PID:g409015
C;Superfamily: tetranectin; C-type lectin homology
F;39-170/Domain: C-type lectin homology <LCH>
A; Molecule type: protein A; Residues: 23-47 < DEC>
                                                                                                                                                                                                                                                 A; Molecule type: protein A; Residues: 23-52; 160-166 < ITO>
                                                                                                                                                                                                                                                                                                             A; Accession: S12950
                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-166 <TER>
A;Residues: 1-166 <TER>
A;Cross-references: GB:M18963; NID:g190978; PIDN:AAA36558.1; PID:g190979
R;Irob, T.; Tsuzuki, H.; Katoh, T.; Teraoka, H.; Matsumoto, K.; Yoshida, FEBS Lett. 272, 85-88, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P05451; GB:J05412 R;Terazono, K.; Yamamoto, H.; Takasawa, S.; S)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-166 <WAT>
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34.5%; Pred. No. 3.6e-15;
tive 25; Mismatches 57
                                                                                                                                                                                                                                                                                                                                            human reg protein PMID:2226837
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de Caro, J.;

Bonicel,

J.; Rovery,

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Caro, A.

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pancreatic stone protein precursor - human C;Species: Homo sapiens (man) C;Jate: 03-Jun-1993 #sequence_revision 03-Jun-1993 C;Accession: A45751 R;Giorgi, D.; Bernard, J.P.; Rouquier, S.; Iovanna, J. Clin. Invest. 84, 100-106, 1989 A;Reference number: A45751; MUID:89292148; PMID:252
                                                                                                                                                                                                                    RESULT 12
A45751
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A;Aross-references: GDB:132455; OMIM:167770
A;Map position: 2p12-2p12
A;Introns: 22/1; 61/3; 107/3; 145/1
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: glycoprotein; lectin; pancreas; pyroglutamic acid
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-166/Product: regenerating islet lectin 1-alpha #status experimental <MAT>
F;34-166/Product: pancreatic stone protein #status experimental <MAT2>
F;36-162/Domain: C-type lectin homology <LCH>
F;36-162/Domain: C-type lectin homology <LCH>
F;33-34/Cleavage site: pyrrolidone carboxylic acid (Gln) (in mature form) #status
F;37-Binding site: carbohydrate (Thr) (covalent) #status experimental
F;33-34/Cleavage site: Arg-Ile (trypsin) #status experimental
F;36-47,64-162,137-154/Disulfide bonds: #status experimental
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A;Residues: 33-48 <RO2>
R;Montalto, G.; Bonicel, J.; Multigner, L.; Rovery, M.; Sarles,
Biochem. J. 238, 227-232, 1986
A;Title: Partial amino acid sequence of human pancreatic stone pareference number: A25246; MUID:87099950; PMID:3541906
A;Accession: A25246
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A; Residues: 63-72;125-139;150-157;160-166 < ROU>
A; Residues: 63-72;125-139;150-157;160-166 < ROU>
A; Note: disulfide bonds
R; de Caro, A.M.; Bonicel, J.J.; Rouimi, P.; de Caro, J.D.;
Bur. J. Biochem. 168, 201-207, 1987
A; Title: Complete amino acid sequence of an immunoreactive
A; Reference number: S00113; MUID:88029417; PMID:3665916
A; Accession: S00113
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A;Molecule type: protein
A;Residues: 34-73,'X',75-87,'R',89-98 <MON>
C;Comment: This protein is found in pancreatic calculi of mammals. The tryptic-like clear C;Comment: Intact regenerating islet lectin 1-alpha, lithostathine, inhibits the growth
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. Clin. Invest. 84, 100-106, 1989;Title: Secretory pancreatic stone protein messenger RNA.;Reference number: A45751; MUID:89292148; PMID:2525567
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S02419; MUID:88152214; PMID:3345835
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                                                                                     J.; Sarles,
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                                                                                     J.C.
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pancreatitis-associated protein precursor - human N,Alternate names: C-type lectin; pancreatic stone protein homolog HIP C;Species: Homo sapiens (man) C;Date: 20-Feb-195 #sequence revision 20-Feb-1995 #text_change 09-Jul-C;Date: 20-Feb-195 #sequence revision 20-Feb-195 #text_change 09-Jul-C;Accession: A49616; A44931; S29821; S48197; I55880 R;Dusetti, N.J.; Frigerio, J.M.; Fox, M.F.; Swallow, D.M.; Dagorn, J.C. Genomics 19, 108-114, 1994 A;Title: Molecular cloning, genomic organization, and chromosomal local A;Reference number: A49616; MUID:94245143; PMID:8188210 A;Accession: A49616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q02988; EMBL:X69062; NID:g64257; C;Superfamily: tetranectin; C-type lectin homology F;37-164/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Isolation and characterization of A; Reference number: $32489; MUID:93279340; A; Accession: $32489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Pleurodeles waltlii (Iberian ribbed newt)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #
C;Accession: S32489; S28530
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S32489
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A;Status: preliminary; not compared with A;Molecule type: mRNA
A;Residues: 1-166 <GIO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Tiffoche, C.; Chesnel, A.; Jego, I
Eur. J. Biochem. 213, 901-907, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-172 <TIF>
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33.3%;
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Pred. No. 9.4e-15;
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PMID:8504829
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                                                                           localization
                                                                                                                  J.C.; Iovanna,
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A;Residues: 1-175 <DUS>
A;Cross-references: UNIPROT:Q06141; GB:L15533; NID:g482908; PIDN:AAA60020.1; A;Cross-references: UNIPROT:Q06141; GB:L15533; NID:g482908; PIDN:AAA60020.1; A;Lasserre, C.; Christa, L.; Simon, M.T.; Vernier, P.; Brechot, C. Cancer Res. 52, 5089-5095, 1992
Cancer Res. 52, 5089-5095, 1992
A;Title: A novel gene (HIP) activated in human primary liver cancer.
    agkisacutacin alpha chain precursor - sharp-nosed v
N;Alternate names: fibrinogenlytic venom protein
C;Species: Agkistrodon acutus (bharp-nosed viper)
C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000
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A;Introns: 26/1; 65/3; 111/3; 154/1
C;Superfamily: tetranectin; C-type
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A;Residues: 1-175 < LA2>
A;Residues: 1-175 < LA2>
R;Orelle, B; Keim, V.; Masciotra, L.; Dagorn, J.C.; Iovanna, J.Clin. Invest. 90, 2284-2291, 1992
A;Title: Human pancreatitis-associated protein. Messenger RNA
A;Reference number: I55580; MUID:93107309; PMID:1469087
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R;Lasserre, C.; Simon, M.T.; Ishikawa, H.; Diriong, S.; Nguyen, V.C.; Christa, Eur. J. Biochem. 224, 29-38, 1994
A;Title: Structural organization and chromosomal localization of a human gene A;Reference number: S48197; MUID:94357229; PMID:8076648
A;Accession: S48197
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A;Title: Cloning and tissue-specific expression of cDNAs
A;Reference number: S29821; MUID:93176807; PMID:7679928
A;Accession: S29821
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A; Residues: 1-175 < ITO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:S51768; NID:g262368; PIDN:AAB24642.1; PID:g262369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-175 <RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Note: sequence extracted from NCBI backbone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-175 < LAS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Superfamily: tetranectin; C-type lectin homology; Superfamily: tetranectin; C-type lectin homology; Pancreas; Reywords: acute phase; extracellular protein; pancreas; 1-26/Domain: signal sequence #status predicted <51G-27-175/Product: pancreatitis-associated protein #status predicted; 40-171/Domain: C-type lectin homology <LCH-27-175/Fromain: C-type lectin homology <LCH-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Status: preliminary; translated from GB/EMBL/DDBJ;Molecule type: mRNA
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10 LLLSCL-AKTGVLGDIIMR--PS----CAPGWFYHKSNCYGYFRKLRNWSDAELECQSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGAHLASILSLKEASTIAEYISGYQRSQP-IWIGLHDPQKRQQ-----WQWIDGAMYLYR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SG-NLVSVLSGAEGSFVSSLVKSIGNSYSYVWIGLHDPTQGTEPNGEGWEWSSSDVMNYF
                                                                                                                                                                                                                                                                                                                                                       AWERNPSTISSPGHCASLSRSTAFLRWKDYNCNVRLPYVCKF
                                                                                                                                                                                                                                                                                                                                                                                                                                   SW--SGKSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKY 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2e-14;
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#text_change 09-Jul-2004
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A;Cross-references: UNIPROT:Q9DEF9; UNIPROT:Q9IAM1; 1
A;Experimental source: venom gland
A;Accession: PC7037
A;Molecule type: protein
A;Residues: 24-53;84-86;87-94;125-136;137-152 <CH2>
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: disulfide bond; heterodimer; venom
F;1-23/Domain: signal sequence #status predicted <SI(F;24-152/Product: agkisacutacin alpha chain #status)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: JC7134; PC7037
R;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J. Biochem. Biophys. Res. Commun. 265, 530-535, 1999
A;Title: Purification, characterization, and cDNA cloning of a new A;Reference number: JC7134; MUID:20025379; PMID:10558903
A;Accession: JC7134
A;Molecule type: mRNA
A;Residues: 1-152 <CHE>
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es 47; Conserv
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                                           126 NKHCAEMSSNNNFLTWSSNECNKRQHFLCK 155
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SKKCLGVHIETGFHKWENFYCEQQDPFVCE 151
                                                                                                                             ILSLKEASTIAEYISGYQRSQPI--WIGLHDPQKRQQW--QWIDGAMYLYRSWSGKSMGG 125
                                                                                                                                                                        LLVVFLSLSGTAAD-----CSSGWSSYEGHCYKVFKQSKTWADAESFCTKQVNGGHLVS
                                                                                  IESSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQCSIEWSDGSSISYENWIEEE---
                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                               26;
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Pred. No. 4.5e-13;
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Search completed: February 11, 2005, 23:43:48
Job time: 40 secs

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Title:
Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                               Score
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1: /cgn2=6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

3: /cgn2=6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2=6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

5: /cgn2=6/ptodata/1/pubpaa/US07 NEW PUB.pep:*

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9: /cgn2=6/ptodata/1/pubpaa/US09 PUBCOMB.pep:*

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11: /cgn2=6/ptodata/1/pubpaa/US09E PUBCOMB.pep:*

12: /cgn2=6/ptodata/1/pubpaa/US09E PUBCOMB.pep:*

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16: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

17: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

18: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*

19: /cgn2=6/ptodata/1/pubpaa/US10 NEW PUB.pep:*
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Gapop 10.0 , Gapext 0.
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1053.599 Million cell updates/sec
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US-09-922-217-1079
US-09-923-217-1079
US-09-933-263-1077
US-09-833-263-1078
US-09-833-263-1078
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US-09-833-263-1080
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Sequence 1070, Ap
Sequence 1077, Ap
Sequence 1078, Ap
Sequence 1079, Ap
Sequence 1070, Ap
Sequence 1070, Ap
Sequence 1077, Ap
Sequence 1078, Ap
Sequence 1079, Ap
Sequence 1079, Ap
Sequence 2, Appli
Sequence 4471, Ap
Sequence 1070, Ap
                                                                                                                                                                                                                                               Description
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                                                                                                                           ; ORGANISM: Homo sapiens US-09-922-217-1070
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US-09-922-217-1070
                                                     Query Match
Best Local Similarity
Matches 158; Conserv
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Result No.

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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Jiang, Yuqiu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: OP COLON CANCER AND METHODS FOR THEIR OF INVENTION: OP COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/9/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEG ID NOS: 1124
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1070
LENGTH: 158
TYPE: PRT
ORGANICA
                                                                                                                                                                                                                                                                                                                                                Sequence 1070, Application US/09922217 Patent No. US/0020076414A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 878; DB 9; Length 158; ilarity 100.0%; Pred. No. 3.8e-82; Conservative 0; Mismatches 0; Indels
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4 US-10-100-6/89-2
4 US-10-105-03-114
4 US-10-205-8-3-3-7
13-8
5 US-10-295-027-781
5 US-10-295-027-781
5 US-10-295-027-781
6 US-10-106-699-639
6 US-10-106-699-639
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6 US-10-28-248-113
7 US-10-108-248-113
7 US-10-108-248-113
8 US-10-108-248-113
8 US-10-108-248-113
8 US-10-108-248-113
9 US-10-108-248-128
9 US-10-108-248-128
9 US-10-108-248-128
9 US-10-108-248-128
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US-10-025-280-1078
US-10-025-380-1079
US-10-025-380-1080
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Sequence 1078, Ap
Sequence 1079, Ap
Sequence 1180, App
Sequence 134, App
Sequence 134, App
Sequence 136, App
Sequence 100, App
Sequence 105, App
Sequence 105, App
Sequence 20, Appli
Sequence 3, Appli
Sequence 113, App
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US-09-922-217-1077
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                                                                                                                                                          Sequence 1078, Application Patent No. US20020076414A1 GENERAL INFORMATION:
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Best Local Similarity 100.
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APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1077
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ORGANISM: Homo sapiens
-09-922-217-1077
              APPLICANT:
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                                      Stolk, John A. Wang, Tongtong
           Jiang, Yuqiu
Smith, Carole Lynn
                                                           Meagher, Madel
Stolk, John A.
                                                                         Secrist, Heather
Benson, Darin R.
Meagher, Madeleine
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Smith, Carole Lynn
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Stolk, John A.
Wang, Tongtong
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Benson, Darin R.
King, Gordon E.
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APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1078
SEQ ID NO 1078
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SEQ ID NO 1079
LENGTH: 158
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Best Local Similarity
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APPLICANT: Sect
APPLICANT: Bent
APPLICANT: Meac
APPLICANT: Stol
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APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USB
TILE REFERENCE: 210121.471C13
CURRENT FILING DATE: 2001-08-03
UNMBER OF SEQ ID NOS: 1124
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TYPE: PRT
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Lodes, Michael J.
Secrist, Heather
Benson, Darin R.
  YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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Stolk, John A.
Wang, Tongtong
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APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: King, Gordon E.
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: OP COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT APPLICATION NUMBER: US/09/922,217
CURRENT FILING DATE: 2001-08-03
NUMBER OF EGO ID NOS: 1124
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-922-217-1080
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US-09-833-263-1070
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; ORGANISM: Homo sapiens
US-09-922-217-1080
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                                                 APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Clapper, Jonathan D.
APPLICANT: Scolk, John A.
APPLICANT: Meagher, Madelaine J.
APPLICANT: Meagher, Madelaine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT APPLICATION NUMBER: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARB: FASTSEQ for Windows Version 3.0
SEQ ID NO 1070
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Best Local Similarity
Matches 158; Conserv
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Patent No. US20020076414A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                       LENGTH: 158
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sal Similarity 100.0%; Pred. No. 3.8e-82;
158; Conservative 0; Mismatches 0;
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Benson, Darin R.
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Sequence 1077, Application US/09833263
; Batent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aljun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Stolk, John A.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOPTWARE: FRATSEQ for Windows Version 3.0
; TYPE: PRT
CREATION OF SEA OF S
Sequence 1078, Application US/09833263

Patent No. US20020110547A1

GENERAL INFORMATION:

APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
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US-09-833-263-1079
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; ORGANISM: Homo
US-09-833-263-1078
                                                                                                                                                                                                   RESULT 10
                                                               Sequence 1080, Application US/09833263
Patent No. US20020110547A1
GENERRAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
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SEQ ID NO 1078
LENGTH: 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1079, Application US/09833263 Patent No. US20020110547A1
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Best Local
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SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-04-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY
TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.471C12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jo
                                               APPLICANT: Meagher, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 100.0%; Score 878; DB 9; Local Similarity 100.0%; Pred. No. 3.8e-82;
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Clapper, John A.
Stolk, John A.
Meagher, Madeleine J.
Meagher, Madeleine J.
Meagher, Madeleine J.
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Pred. No. 3.8e-82;
); Mismatches 0;
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CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 09/162,508
PRIOR FILING DATE: 1998-09-29
PRIOR APPLICATION NUMBER: US 08/468,413
PRIOR PILING DATE: 1995-06-06
NUMBER OF SEO ID NOS: 6
SOFTWARE: Patentin version 3.0
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CURRENT FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 1080
                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 158
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Best Local Similarity 100.0%;
Matches 158; Conservative 0
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                Best
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TITLE OF INVENTION: Colon Specific Gene and Protein
FILE REFERENCE: PF17802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER AND METHODS FOR THEIR USE FILE REFERENCE: 210121.471C12
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 158
TYPE: PRT
                                                                                                                                                                                                                                            Local Similarity
121
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                                                                                                                                                      1 MAŚRŚMRLLLLLŚCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                   KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                              YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAWYLYRSWSG 120
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KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                                                                         100.0%; ilarity 100.0%; Conservative 0;
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Pred. No. 3.8e-82;
                                                                                                                                                                                                                         Score 878; DB 10;
Pred. No. 3.8e-82;
); Mismatches 0;
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RESULT 12 US-09-969-034-4471

Sequence 4471, Application US/09969034 Publication No. US20040110668A1

GENERAL INFORMATION:

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APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick Thomas S.

APPLICANT: Carrer, Darrick

TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C14

CURRENT APPLICATION NUMBER: US/10/025,380

CURRENT FILING DATE: 2001-12-19

NUMBER OF SEQ ID NOS: 1129

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1070

LENGTH: 158

TYPE: PRT

ORGANISM: Homo sapiens

US-10-025-380-1070
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TITLE OF INVENTION: Nucleic Acid Sequences Differentially
TITLE OF INVENTION: Expressed in Cancer Tissue
FILE REFERENCE: 1657/1032
CURRENT APPLICATION NUMBER: US/09/969,034
CURRENT FILING DATE: 2001-10-02
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR APPLICATION NUMBER: 60/237,271
PRIOR FILING DATE: 2000-02-10
NUMBER OF SEQ ID NOS: 4494
SOFTWARE: PasetSEQ for Windows Version 4.0
SEQ ID NO 4471
LENGTH: 158
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US-10-025-380-1070
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Best Local Similarity
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Carroll, Eddie III
Catino, Theodore J.
Dwivedi, Poornima
Molino, Gary A.
Thiagalingam, Arunthathi
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Meagher, Mu.
Tk, John A.
Thong
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Smith, Carole L.
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Benson, Darin R.
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Wang, Aijun
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1, Eddie III
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APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Vedvick Thomas S.
APPLICANT: Vedvick Thomas S.
APPLICANT: Or CATTER, DATRICK
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT APPLICATION SEQ 101-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTMARE: FASISEQ for Windows Version 4.0
SEQ ID NO 1077
LENGTH: 158
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-025-380-1077
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APPLICANT: Ku, Jiangchun
APPLICANT: Lodes, Michael
APPLICANT: Secrist, Heath
APPLICANT: Benson, Darin
APPLICANT: Meagher, Madel
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Best Local Similarity 100.
Matches 158; Conservative
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APPLICANT:
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Benson, Darin R.
Meagher, Madeleine J
Stolk, John A.
Wang, Tongtong
                         KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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                                                                       YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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Smith, Carole L.
King, Gordon B.
Wang, Aijun
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 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP
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Pred. No. 3.8e-82;
0; Mismatches 0;
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RESULT 15 US-10-025-380-1078 ; Sequence 1078, Application US/10025380 ; Publication No. US20020182191A1

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APPLICANT: Clapper, Jonathan D.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Skeiky, Yasir A. W.
APPLICANT: Panger, Gary R.
APPLICANT: Vedvick Thomas S.
APPLICANT: Vedvick Thomas S.
APPLICANT: Vedvick Thomas S.
APPLICANT: Corter, Darrick
FIITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025,380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 1078
LENGTH: 158
TYPE: PRT
ORGANISM: Homo sapiens
Search completed: February 11, 2005, 23:33:33 Job time : 50 secs
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APPLICANT: Ku, Jiangchun
APPLICANT: Lodes, Michael
APPLICANT: Lodes, Michael
APPLICANT: Secrist, Heath
APPLICANT: Secrist, Margher, Madel
APPLICANT: Meagher, Madel
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Tongtong
APPLICANT: Smith, Carole
APPLICANT: King, Gordon B
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonat
APPLICANT: Skeiky, Yasir
APPLICANT: Seiky, Yasir
APPLICANT: Carter, Darric
APPLICANT: Carter, Darric
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                                                                                   121 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
                                                                                                                                                                        61 YGNGAHLASILSLKEASTIAEYISGYORSOPIWIGLHDPQKROOWOWIDGAMYLYRSWSG 120
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Secrist, Heather
Benson, Darin R.
Meagher, Madeleine Joy
Stolk, John A.
Wang, Tongtong
Jiang, Yuqiu
Smith, Carole L.
King, Gordon E.
Wang, Aijun
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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-621-976-4812
US-08-401-530A-7
US-08-729-103-3
US-08-729-103-3
US-08-729-103-4
US-09-949-016-16686
US-08-401-530A-5
US-08-401-530A-6
US-08-401-530A-6
US-08-709-662-6
US-08-709-662-6
US-09-949-016-10685
US-09-949-016-10685
        US-08-464-637-2

US-08-401-530A-4

US-08-709-662-4

US-08-822-261-3

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US-07-778-156-7

US-08-822-261-4
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US-08-468-413-2
US-09-162-508-2
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       Sequence 1, Appli
Sequence 2, Appli
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Sequence 4, Appli
Sequence 7, Appli
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Sequence 6, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 6, Appli
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Sequence 10685, Appli
Sequence 10685, Appli
Sequence 2, Appli
Sequence 3, Appli
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Sequence 4, Appli
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Sequence 3, Appli
Sequence 10537, Appli
Sequence 7, Appli
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8	218	24.8	174	4.	US-09-226-852-4	Sequence 4
29	208	23.7	175	N	US-08-401-530A-3	ø
ö	208	•	175	N	US-08-709-662-3	Φ
3	204.5	23.3	130	<u>,,,</u>	US-07-893-929A-7	Sequence 7
2	204.5	٠	130	v	PCT-US92-10344-7	Sequence 7,
ພ	204	•	175	N	US-08-822-261-1	Sequence 1
34	204	23.2	175	4	US-09-226-852-1	Sequence 1
35	198.5	•	132	۲	US-07-893-929A-5	
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37	198.5		134	۲	US-07-893-929A-2	O
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4	190	•	174	N	US-08-401-530A-2	æ
55	190	2	174	v	TTC_00_700_663_3	D

ALIGNMENTS

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US-08-729-103-1
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                                                                                                                                TELEPHONE: 415-855-0555
TELEPHONE: 415-845-4166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1 Application US/08729103

Patent No. 38378412.

GENERAL INFORMATION:

APPLICANT: —Bandman, Olga
APPLICANT: Goll, Surya K.

TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOPTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,103
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                   PILING DATE:
ATTORINEY AGENT INFORMATION:
ATTORINEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGERENCE/DOCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                  STRANDEDNESS: 8
TOPOLOGY: 1inea
MOLECULE TYPE: pe
IMMEDIATE SOURCE:
LIBRARY: COLNFE
CLONE: 1310334
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ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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3174 Porter Drive
                                         COLNFET 02
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Query Match Best Local Similarity

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Mismatches

100.0%; Score 878; DB 2; 100.0%; Pred. No. 5.9e-88;

Length 158; Indels

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Gaps

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Matches 158;

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US-08-468-413-2
                                                                                                                                                                                                                                                                                     TELEPÄX: 201-994-1700
INFORMATIÓN FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 158 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
08-468-413-2
                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 158; Conserv
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APPLICANT: LI, ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRAPTON NUMBER: 36,114
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201,994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/466
FILING DATE: 06 JUN 95
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION JOMBER:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN, ADDRESSEE: CECCHI, STEWART & OLSTEIN STREET: 6 BECKER FARM ROAD CITY: ROSELAND STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PS,
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE
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                      KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
                                                                                         YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAWYLYRSWSG 120
                                                                                                                                          MASRSMRLLLLLSCLAKTGVLGDI IMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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KSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYRP 158
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                                                                                                                                                                                                               100.0%; Score 878; DB 2; Length 158; ilarity 100.0%; Pred. No. 5.9e-88; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPAX: 201-991-1...
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 158 AMINO ACIDS
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09162508 Patent No. 6080722
                                                                                                                                    Sequence 2, Application PC/TUS9507169 GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/468,41
FILING DATE: 06 JUN 95
ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERENCE/DOCKET NUMBER: 3258
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/162,508
APPLICANT: LI, ET AL.
TITLE OF INVENTION: Human Colon Specific Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: CEARELLA, BEYANE, BAIN, GILFILLAN,
ADDRESSEE: CECHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: HUNDMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: ROSELAND
STATE: NEW JERSEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: CARELLA, BYRNE, BAIN, ADDRESSEE: CECCHI, STEWART & OLS'
                                                                                                                                                                                                                                                                      121 KSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYRP 158
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                                                                                                                                                                                                                                                                                                                                                    61 YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MASRSMRLLLLLLSCLAKTGVLGDIIMRPSCAPGWFYHKSNCYGYFRKLRNWSDAELECQS
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                                                                                                                                                                                                                                                                                                                                YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 878; DB 3;
Pred. No. 5.9e-88;
); Mismatches 0;
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                                                                                                                                                                                                                                                        158
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: ROSELAND E: NEW JERSEY FRY: USA

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; NUMBER OF SEQ ID NOS: 19335
; SEQ ID NO 4812
; SEQ ID NO 4812
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-621-976-4812
                                                                                                                                                                                                                                                                                                                                                                 RESULT 5
US-09-621-976-4812
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Query Match
Best Local Similarity
Matches 122; Conserv
                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                    Sequence 4812, Application US/09621976 Patent No. 6639063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                         APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                              APPLICANT: Dumas Milne Edwards, J.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                            APPLICANT: Jobert, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REFERRENCE/DOCKET NUMBER: 325800-389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 158 AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US:
FILING DATE: 06 JUN 95
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGNGAHLASILSLKEASTIAEYISGYQRSQPIWIGLHDPQKRQQWQWIDGAMYLYRSWSG 120
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       Conservative
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06 JUN 95
                  79.2%; Score 695; DB 4; 100.0%; Pred. No. 3.9e-68;
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     Mismatches
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                                     Length 122;
     Indels
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US-08-401-530A-7
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                                                                                                                                                                                          Query Match 29.0%; Score 254.5; DB 2; Best Local Similarity 30.6%; Pred. No. 6.6e-20; Matches 52; Conservative 38; Mismatches 51;
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APPLICANT:
APPLICANT:
APPLICANT:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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APPLICANT: Duguid, William P.
TITLE OF INVENTION: INCAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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CLASSIFICATION: 800
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STREET: 1001 G Street, N.W.
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110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
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), 5834590
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                                                                             SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
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                                                       AEADLFCONWINSG-YLVSVLSQAEGNFLASLIKESGTTAAN-VWIGLHDPKINRRWHWSS 114
                                                                                                                         KYFILLSCL-----MVLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW 56
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                                                                                                                                                                                                                              DB 2;
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; Sequence 7, Application US/08709662
Patent No. 5840531
; GENERAL INFORMATION:
; APPLICANT: Vinik, Aaron I.
; APPLICANT: Pittenger, Gary L.
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US-08-709-662-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 393209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
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APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                   52 SDAELECQSYGNGAHLASILSLKEASTIAEYI--SGYQRSQPIWIGLHDPQKRQQWQWID 109
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                                                                                                                                                                                                                                                                                                                                                            7 RLLLLLSCLAKTGVLGDIIMRPS------CAPGWFYHKSNCYGYFRKLRNW 51
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                                                                                                                                                                     GSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKWRDNSCDAQLSFVCKFK 164
                                                                                                                                                                                                                                                                                                                        KYFILLSCL-----MVLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW 56
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                                                                                                                                                                                                                                                                                                                                                                                               29.0%; Score 254.5; DB 2; 30.6%; Pred. No. 6.6e-20; tive 38; Mismatches 51;
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Patent No. 5837841
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                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Bandman, Olga
APPLICANT: GOLI, Surya K.
TITLE OF INVENTION: NOVEL HUMAN REG PROTEIN
NUMBER OF SEQUENCES: 4
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ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 165 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US/08/709,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OP INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
 COMPUTER READABLE FORM:
                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                  STREET: 3174 Por
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Kagan, Sarah A. REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                   COUNTRY: UZIP: 94304
                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 09-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 29.0%;
Local Similarity 30.6%;
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                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-508-9100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                              115
                                                                                                                                                                                                                                                                                                                                                                                                 110 GAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157
                                                                                                                                                                                                                                                                                                                                                                                                                                       57 AEADLFCONMNSG-YLVSVLSQAEGNFLASLIKESGTTAAN-VWIGLHDPKNNRRWHWSS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          52 SDAELECQSYGNGAHLASILSLKEASTIAEYI -- SGYQRSQPIWIGLHDPQKRQQWQWID 109
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                                                                                                                                                                                                                                                                                                                                                              GSLFLYKSWDTGYPNNSNRGYCVSVTSNSGYKKWRDNSCDAQLSFVCKFK 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KYFILLSCL-----MVLSPSQGQEAEEDLPSARITCPEGSNAYSSYCYYFMEDHLSW
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                                                                                          E: Incyte Pharmaceuticals, 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Banner & Witcoff, Ltd.
1001 G Street, N.W.
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DN: 435
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Pred. No. 6.6
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6.6e-20; DB 2; 51;

Length 165; Indels

29;

Gaps

OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version 1.5

: Diskette IBM Compatible

MEDIUM TYPE:

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US-08-729-103-4
                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
                                                                                                                                    SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10686
LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10686, Application US/09949016 Patent No. 6812339
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Best Local (
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VENTER, J.
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOI307
                                                                      ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 4:
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LLERARY: GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 166 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 27.3%; Score 240; DB 2; Length 166; Local Similarity 34.3%; Pred. No. 2.6e-18; see 46; Conservative 27; Mismatches 57; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 ESCEKKFSFVCKFK 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         166 amino acids
27.3%;
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Score 240; DB 4; Length 174; Pred. No. 2.7e-18;
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US-08-401-530A-5
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APPLICANT: Vinik,
APPLICANT: Pitteng
APPLICANT: Rafaelo
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                                                                                                                                                                Matches
                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: KAGAIN, SATAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 005
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
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APPLICANT:
                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Rattus rati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
CLASSIFICATION: 800
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CITY: W
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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ZIP: 20001-4597
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STREET: 1001 G Street, N.W.
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160 ESCEKKFSFVCKFK 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5, Application US/08401530A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87 QRSQP-IWIGLHDPQKRQQWQWIDGAMYLYRSW-SGKSMGGNK-HCAEMSSNNNFLTWSS 143
65 DLACOKRPSG-HLVSVLSGSEASTVSSLIKSSGNSGQNVWIGLHDPTLGQEPNRGGWEWS 123
                                       55 ELECQSYGNGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDPQKRQQ-----WQWI 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 RPSCAPGWFYHKSNCYGYFRKLRNWSDAELECOSYGNGAHLASILSLKEASTIAEYISGY 86
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D.C
                                                                               VALTTMSWMLLSSLMLLSQVQGEDAKEDVPTSRISCPKGSRAYGSYCYALFSVSKSWFDA
                                                                                                                      MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                            174 amino acids
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Rafaeloff, Ronit
                                                                                                                                                              26.3%; Score 231; DB 2; Length 174; ilarity 32.4%; Pred. No. 2.6e-17; Conservative 28; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vinik, Aaron I.
                                                                                                                                                                                                                                                                          Rattus rattus
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                                                                                                                                                                  Indels 14;
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109

DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKRQHFLCKYR 157

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RESULT 13
US-08-401-530A-6
US-08-401-530A-6
; Sequence 6, Application US/08401530A
; Patent No. 5834590
; Patent No. 5834590
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US-08-709-662-5
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Best Local S
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,662
FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rosenberg, Lawrence
APPLICANT: Duguid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1001 G S CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Banner & Witcoff, Ltd.
STREET: 1001 G Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                      124 NADVMNÝFNWETNPSSVSGSHCGTLTRASGFLRWRENNCISELPYVCKFK 173
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                                                                                                                                                                                                                                                                                         1 MASRSMRLLLLLSCLAKTGVLGD-----IIMRPSCAPGWFYHKSNCYGYFRKLRNWSDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
OGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20001-4597
                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                   DGAMYLYRSW-SGKSMGGNKHCAEMSSNNNFLTWSSNECNKROHFLCKYR 157
                                                                                                                                                                                                             ELECQSYGNGAHLASILSLKEASTIAEYI-SGYQRSQPIWIGLHDPQKRQQ-----WQWI 108
                                                                                                                                                                                      DLACOKRPSG-HLVSVLSGSBASFVSSLIKSSGNSGONVWIGLHDPTLGOEPNRGGWEWS 123
                                                                                                                                                                                                                                                         VALTTMSWMLLSSLMLLSQVQGEDAKEDVPTSRISCPKGSRAYGSYCYALFSVSKSWFDA
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Rafaeloff, Ronit
                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              Rattus rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                           26.3%; Score 231; DB 2; Length 174; 32.4%; Pred. No. 2.6e-17;
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US-08-709-662-6
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US-08-401-530A-6
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Sequence 6, Appir....

Patent No. 5840531

Patent No. 5840531

ORNERAL INFORMATION:

Ulnik, Aaron I.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,530A
FILING DATE: 22-FEB-1995
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REGISTRATION NUMBER: 32,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                         APPLICANT: Vinik, Aaron 1.
APPLICANT: Pittenger, Gary L.
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rafaeloff, Ronit
APPLICANT: Rogenberg, Lewrence
APPLICANT: Dugnid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
TITLE OF INVENTION: ISLET NEOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: I
ORIGINAL SOURCE:
ORGANISM: Ratt
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APPLICANT:
APPLICANT:
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ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Duguid, William P.
TITLE OF INVENTION: INGAP PROTEIN INVOLVED IN PANCREATIC
TITLE OF INVENTION: ISLET NEOGENESIS
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
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    ADDRESSEE:
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1001 G Street, N.W.
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Rafaeloff, Ronit
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Banner & Witcoff, Ltd.
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STREET:

Washington

1001 G Street, N.W.

D.C.

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; ORGANISM: Human US-09-949-016-10685
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                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 26.0%; Score 228.5; DB 2; Best Local Similarity 34.5%; Pred. No. 4.9e-17; Matches 48; Conservative 25; Mismatches 57;
                                                               NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 10685
LENGTH: 144
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10685, Application US/09949016 Patent No. 6812339
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FILING DATE: 09-SEP-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGSAN, SATAh A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 0057
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRI
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/709,662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Rattus ratt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 174 amino acid
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TYPE: amino acid
TOPOLOGY: linear
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LKWGDHHCDVELPFVCKFK 173
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                                                                                                                  for Windows Version
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Search completed: February 11, 2005, 23:43:03 Job time : 44 secs

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